











Related Structures

Sequences producing significant alignments:			Score (bits)	E Value	
gi 7019846 dbj BAA90893.1 	unnamed protein product [Homo sa...	677	0.0		
gi 31542986 ref NP_060095.2 	intelectin; endothelial lectin...	674	0.0		
gi 37724005 gb AAO17800.1 	intelectin [Homo sapiens]	672	0.0		
gi 18254480 ref NP_543154.1 	intelectin 2; endothelial lect...	562	e-159		
gi 6754388 ref NP_034714.1 	intelectin [Mus musculus] >gi 7...	554	e-156		
gi 28932914 gb AAO60215.1 	intelectin 2 [Mus musculus]	540	e-152		
gi 45360437 ref NP_988929.1 	hypothetical protein MGC76330 ...	438	e-121		
gi 20502359 dbj BAB91359.1 	35 kDa serum lectin [Xenopus la...	428	e-118		
gi 28971732 dbj BAC65329.1 	embryonic epidermal lectin [Xen...	426	e-118		
gi 20502361 dbj BAB91360.1 	lectin type 2 [Xenopus laevis]	419	e-116		
gi 49255965 gb AAH71079.1 	Unknown (protein for MGC:79927) ...	408	e-112		
gi 2632076 emb CAA57946.1 	cortical granule lectin [Xenopus...	408	e-112		

gi 1841845 gb AAB47537.1	lectin [Xenopus laevis]	406	e-112	
gi 49115332 gb AAH73311.1	Unknown (protein for MGC:80711) ...	400	e-110	
gi 45360965 ref NP_988850.1	egg cortical granule lectin [X...	399	e-110	
gi 13094239 dbj BAB32787.1	serum lectin [Lethenteron japon...	346	7e-94	
gi 1079283 pir S49589	cortical granule lectin - African cl...	330	5e-89	
gi 11095793 gb AAG30025.1	putative interlectin [Oncorhynch...	117	7e-25	
gi 31196141 ref XP_307018.1	ENSANGP00000016440 [Anopheles ...	48	4e-04	
gi 42524002 ref NP_969382.1	hypothetical protein predicted...	47	6e-04	
gi 42524003 ref NP_969383.1	hypothetical protein predicted...	46	0.001	
gi 120092 sp P19477 FIBA_PARPA	Fibrinogen-like protein A pr...	44	0.007	
gi 34853459 ref XP_342180.1	similar to Rho-guanine nucleot...	44	0.009	
gi 4505065 ref NP_003541.1	MAD1-like 1; MAD1 (mitotic arre...	43	0.016	
gi 47086505 ref NP_997939.1	Unknown (protein for MGC:77116...	42	0.021	
gi 31200947 ref XP_309421.1	ENSANGP00000011252 [Anopheles ...	40	0.10	
gi 41107704 ref XP_031401.4	EGF-like-domain, multiple 3 [H...	39	0.18	
gi 42820328 emb CAF31637.1	keratin associated protein 5-8 ...	39	0.23	
gi 47210774 emb CAF90667.1	unnamed protein product [Tetrao...	39	0.30	
gi 47225870 emb CAF98350.1	unnamed protein product [Tetrao...	39	0.30	
gi 38372386 sp Q9BYQ1 KR95_HUMAN	Keratin associated protein...	39	0.30	
gi 28875408 gb AAO59918.1	fibrinogen related protein 12.1 ...	38	0.39	
gi 28875410 gb AAO59919.1	fibrinogen related protein 12.1-...	38	0.39	
gi 399492 sp P02675 FIBB_HUMAN	Fibrinogen beta chain precur...	38	0.39	
gi 11761631 ref NP_005132.1	fibrinogen, beta chain preprop...	38	0.39	
gi 223002 prf 0401173A	fibrin beta	38	0.39	
gi 182430 gb AAA52429.1	beta-fibrinogen precursor	38	0.39	
gi 2781208 pdb 1FZA B	Chain B, Crystal Structure Of Fibrino...	38	0.39	
gi 24987624 pdb 1LT9 B	Chain B, Crystal Structure Of Recomb...	38	0.39	
gi 49258694 pdb 1RE3 B	Chain B, Crystal Structure Of Fragme...	38	0.39	
gi 47217467 emb CAG10236.1	unnamed protein product [Tetrao...	38	0.51	
gi 47479508 gb AAH69560.1	KRTAP9-2 protein [Homo sapiens]	38	0.51	
gi 46395624 sp O75095 EFL3_HUMAN	Multiple EGF-like-domain p...	38	0.51	
gi 38372389 sp Q9BYQ4 KR92_HUMAN	Keratin associated protein...	38	0.51	
gi 16118240 ref NP_114167.2	keratin associated protein 9.2...	38	0.51	
gi 30409360 dbj BAC76375.1	ficolin-1 [Xenopus laevis]	37	0.67	
gi 34880777 ref XP_222794.2	similar to tenascin-N [Rattus ...	37	0.67	
gi 30409366 dbj BAC76378.1	ficolin-4 [Xenopus laevis]	37	0.87	
gi 30409362 dbj BAC76376.1	ficolin-2 [Xenopus laevis]	37	0.87	
gi 46806224 dbj BAD17448.1	hypothetical protein [Oryza sat...	37	0.87	
gi 28195390 ref NP_689829.2	tripartite motif-containing 42...	37	1.1	
gi 30316326 sp P02678_2	[Segment 2 of 2] Fibrinogen beta c...	37	1.1	
gi 37359684 emb CAE47765.1	SI:bZ1P14.8.1 (novel protein si...	37	1.1	
gi 7441528 pir A25052	fibrinogen beta chain - sea lamprey ...	37	1.1	
gi 21757165 dbj BAC05042.1	unnamed protein product [Homo s...	37	1.1	
gi 23200381 pdb 1LWU B	Chain B, Crystal Structure Of Fragme...	37	1.1	
gi 23104420 ref ZP_00090884.1	COG0500: SAM-dependent methy...	37	1.1	
gi 28195392 ref NP_084495.1	tripartite motif-containing 42...	36	1.5	
gi 27754776 ref NP_003656.2	ficolin 3 isoform 1 precursor;...	36	1.5	
gi 37181268 gb AAQ88448.1	NL3 [Homo sapiens]	36	1.5	
gi 13124185 sp O75636 FCN3_HUMAN	Ficolin 3 precursor (Colla...	36	1.5	
gi 30409364 dbj BAC76377.1	ficolin-3 [Xenopus laevis]	36	1.5	

gi 27754778 ref NP_775628.1	ficolin 3 isoform 2 precursor;...	36	1.5	
gi 34858971 ref XP_215890.2	similar to angiopoietin 3 [Rat...	36	1.9	
gi 9229906 dbj BAB00626.1	fibrinogen-like protein [Ciona i...	36	1.9	
gi 6753006 ref NP_033771.1	angiopoietin 4; angiopoietin 3 ...	36	1.9	
gi 47229454 emb CAF99442.1	unnamed protein product [Tetrao...	36	1.9	
gi 47196977 emb CAF88157.1	unnamed protein product [Tetrao...	36	1.9	
gi 38196089 gb AAR13732.1	fibrinogen [Anopheles gambiae]	35	2.5	
gi 31200995 ref XP_309445.1	ENSANGP00000011248 [Anopheles ...	35	2.5	
gi 9280285 dbj BAB01686.1	unnamed protein product [Macaca ...	35	2.5	
gi 46204657 ref ZP_00049663.2	COG0601: ABC-type dipeptide/...	35	2.5	
gi 31199197 ref XP_308546.1	ENSANGP00000015891 [Anopheles ...	35	2.5	
gi 47228399 emb CAG05219.1	unnamed protein product [Tetrao...	35	2.5	
gi 47522525 dbj BAD20197.1	keratin associated protein [Hom...	35	2.5	
gi 13676535 dbj BAB41181.1	hypothetical protein [Macaca fa...	35	2.5	
gi 745664 prf 2016385A sea	anemone toxin Bg II	35	3.3	
gi 16078002 ref NP_388818.1	similar to cell wall-binding p...	35	3.3	
gi 31200937 ref XP_309416.1	ENSANGP00000011265 [Anopheles ...	35	3.3	
gi 34879228 ref XP_344545.1	angiopoietin-2 [Rattus norvegi...	35	3.3	
gi 33859809 ref NP_862897.1	fibrinogen, B beta polypeptide...	35	3.3	
gi 45383970 ref NP_990520.1	tenascin Y variant [Gallus gal...	32	3.5	
gi 8569622 pdb 1EI3 B	Chain B, Crystal Structure Of Native ...	35	4.3	
gi 399491 sp Q02020 FIBB_CHICK	Fibrinogen beta chain precu...	35	4.3	
gi 38372384 sp Q9BYP9 KR99_HUMAN	Keratin associated protein...	35	4.3	
gi 40646583 gb AAR88166.1	aslectin AL-1 [Armigeres subalba...	35	4.3	
gi 7479340 pir T34649	hypothetical protein SC1A11.02c SC1A...	35	4.3	
gi 47209640 emb CAF93081.1	unnamed protein product [Tetrao...	35	4.3	
gi 33598935 ref NP_663327.1	scavenger receptor class F, me...	34	5.6	
gi 21685564 dbj BAC02696.1	SREC-5 [Homo sapiens]	34	5.6	
gi 32041310 ref ZP_00138893.1	COG2087: Adenosyl cobinamide...	34	5.6	
gi 42661152 ref XP_375452.1	similar to keratin associated ...	34	5.6	
gi 13928546 dbj BAB47147.1	complement component C6 [Branch...	34	5.6	
gi 33598927 ref NP_663324.1	scavenger receptor class F, me...	34	5.6	
gi 33598933 ref NP_663326.1	scavenger receptor class F, me...	34	5.6	
gi 33598931 ref NP_663325.1	scavenger receptor class F, me...	34	5.6	
gi 21685560 dbj BAC02694.1	SREC-3 [Homo sapiens]	34	5.6	
gi 3386666 dbj BAA32041.1	D4 dopamine receptor (D4DR) [Tar...	34	5.6	
gi 33598929 ref NP_003684.2	scavenger receptor class F, me...	34	5.6	
gi 20140022 sp Q14162 SREC_HUMAN	Endothelial cells scavenge...	34	5.6	

Alignments

Get selected sequences

Select all

Deselect all



>gi|7019846|dbj|BAA90893.1| unnamed protein product [Homo sapiens]

gi|8096221|dbj|BAA96094.1| intelectin [Homo sapiens]

gi|18091783|gb|AAL58073.1| endothelial lectin HL-1 [Homo sapiens]

gi|20377087|gb|AAM20741.1| intestinal lactoferrin receptor [Homo sapiens]

gi|37181843|gb|AAQ88725.1| ITLN [Homo sapiens]

gi|37724012|gb|AA017801.1|  intelectin [Homo sapiens]
gi|44976129|gb|AAS49907.1|  omentin [Homo sapiens]
gi|48146565|emb|CAG33505.1| ITLN1 [Homo sapiens]
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Score = 677 bits (1747), Expect = 0.0
 Identities = 313/313 (100%), Positives = 313/313 (100%)
 Frame = +1

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 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT
 Sbjct: 1 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60




Query: 283 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY
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Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 642
 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG
 Sbjct: 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV 822
 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV
 Sbjct: 181 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV 240

Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSS 1002
 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSS
 Sbjct: 241 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSS 300

Query: 1003 REITEAAVLLFYR 1041
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 Sbjct: 301 REITEAAVLLFYR 313

 >gi|31542986|ref|NP_060095.2|  intelectin; endothelial lectin HL-1; intestinal
 [Homo sapiens]
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 Frame = +1

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 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT
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

Query: 283 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
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Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 642
 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG
 Sbjct: 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV 822
 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV
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Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYS 1002
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 Sbjct: 1 MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60





Query: 283 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKA YPEGDGNWANY
 Sbjct: 61 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKAVYPEGDGNWANY 120

Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 642
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 Sbjct: 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV 822
 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV
 Sbjct: 181 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV 240

Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYS 1002
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 Sbjct: 241 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYS 300

Query: 1003 REITEAAVLLFY 1038
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 >gi|18254480|ref|NP_543154.1|  intelectin 2; endothelial lectin HL-2 [Homo sapiens]
 gi|18091785|gb|AAL58074.1|  endothelial lectin HL-2 [Homo sapiens]
 gi|37182928|gb|AAQ89264.1|  ITLN2 [Homo sapiens]
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Score = 562 bits (1449), Expect = e-159
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 Frame = +1

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 TM +L FLLF T G S A++ +E+ TC+ S SLPRSCKEIK+ C SA DG
 Sbjct: 7 TMTRLCFLFLFSVATSGCSAAAASSLEMLSREFETCAFSFSSLPRSCKEIKERCHSAGDG 66

Query: 265 LYFLRTENGVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGD 444
 LYFLRT+NGV+YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQG+KADYPEGD

Sbjct: 67 LYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKADYPEGD 126

Query: 445 GNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTG 624
GNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNS+LLRYRT+TG

Sbjct: 127 GNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLRYRTNTG 186

Query: 625 FLQTLGHNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAG 804
FLQ LGHNLFGIYQKYPVKY GKCW DNGP IPVYDFGDA+KTASYSPYQGREF AG

Sbjct: 187 FLQRLGHNLFGIYQKYPVKYRSGKWCNDNGPAIPVVYDFGDAKKTASYSPYQGREFVAG 246

Query: 805 FVQFRVFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTH 984
FVQFRVFNNERAANALCAG++VTGCNTEHHCIGGGG+FP+ P+QCGDFS FDW GYGTH

Sbjct: 247 FVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGDFSADFWDGYGTH 306

Query: 985 VGYSSSREITEAAVLLFYR 1041
V S SREITEAAVLLFYR

Sbjct: 307 VKSSCSREITEAAVLLFYR 325

>gi|6754388|ref|NP_034714.1| [E] intellectin [Mus musculus]
gi|7513698|pir|JE0328 intellectin - mouse
gi|3357909|dbj|BAA31992.1| [E] intellectin [Mus musculus]
gi|12841004|dbj|BAB25043.1| [E] unnamed protein product [Mus musculus]
gi|37724014|gb|AAO17802.1| [E] intellectin [Mus musculus]
gi|37724016|gb|AAO17803.1| [E] intellectin [Mus musculus]
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Score = 554 bits (1427), Expect = e-156
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Frame = +1

Query: 103 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 282
M QL FLLF++ TRG S E N W S SLPRSCKEIK E A DGLYFLRT

Sbjct: 1 MTQLGFLFLFIMVATRGCSAAEENLDTNRWGNSSFSSSLPRSCKEIKQEHTKAQDGLYFLRT 60

Query: 283 ENGVYIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
+NGVYIYQTFCDMT+ GGGWTLVASVHEN+MRGKCTVGDRWSSQQG++ADYPEGDGNWANY

Sbjct: 61 KNGVYIYQTFCDMTTAGGGWTLVASVHENNMRGKCTVGDRWSSQQGNRADYPEGDGNWANY 120

Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 642
NTFGSAEAATSDDYKNPGY+DIQA++LGIWHVPNKSP+ +WR SSLRYRT TGFLQ LG

Sbjct: 121 NTFGSAEAATSDDYKNPGYFDIQAENLGIWHVPNKSPHLNWRKSSLLRYRTFTGFLQHLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV 822
HNLF+Y+KYPVKYGEKGCWTDNGP +PVVYDFGDA+KTASYSPY QGREFTAG+VQFRV


Sbjct: 181 HNLFGLYKKYPVKYGEKGCWTDNGPALPVVYDFGDARKTASYSPSPGQGREFTAGYVQFRV 240

Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSS 1002
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Sbjct: 241 FNNERAASALCAGVRVTGCNTEHHCIGGGGFFPEGNPVQCGDFASFDWDGYGTHNGYSSS 300

Query: 1003 REITEAAVLLFYR 1041
R+ITEAAVLLFYR

Sbjct: 301 RKITEAAVLLFYR 313

 >gi|28932914|gb|AAO60215.1| intelectin 2 [Mus musculus]
Length = 313

Score = 540 bits (1391), Expect = e-152
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Frame = +1

Query: 103 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 282
M QL FLLF++ TR S E N W S SLPRSCKEIK E A DGLYFLRT
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


Query: 283 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
ENGVIYQTFCDMT+ GGGWTLVASVHEN++RG+CTVGDRWSSQQG++ADYPEGDGNWANY
Sbjct: 61 ENGVIIYQTFCDMTTAGGGWTLVASVHENNLGRCTVGDRWSSQQGNRADYPEGDGNWANY 120

Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 642
NTFGSAE ATSDDYKNPGY+DIQA++LGIWHVPN SP+ WRNSSLLRYRT TGFLQ LG
Sbjct: 121 NTFGSAEGATSDDYKNPGYFDIQAENLGIWHVPNNSPHLHTWRNSSLLRYRTFTGFLQRLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV 822
HNLFG+YQKYPVKYGEKGCWTDNGP PVVYDFGDAQKTASYSP G+ EFTAG+VQFRV
Sbjct: 181 HNLFGIYQKYPVKYGEKGCWTDNGPAFPVVYDFGDAQKTASYSPSGRNEFTAGYVQFRV 240

Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSS 1002
FNNERAA+ALCAG+RVTCNTEHHCIGGGG+FPE P++CGDF+ FD +GYGTH+ YS+S
Sbjct: 241 FNNERAASALCAGVRVTGCNTEHHCIGGGGFFPEFDPEECGDFAAFDANGYGTHIRYSNS 300

Query: 1003 REITEAAVLLFYR 1041
REITEAAVLLFYR
Sbjct: 301 REITEAAVLLFYR 313

 >gi|45360437|ref|NP_988929.1|  hypothetical protein MGC76330 [Xenopus tropicalis]
gi|38174756|gb|AAH61445.1|  Hypothetical protein MGC76330 [Xenopus tropicalis]
Length = 339

Score = 438 bits (1126), Expect = e-121
Identities = 210/327 (64%), Positives = 238/327 (72%)
Frame = +1

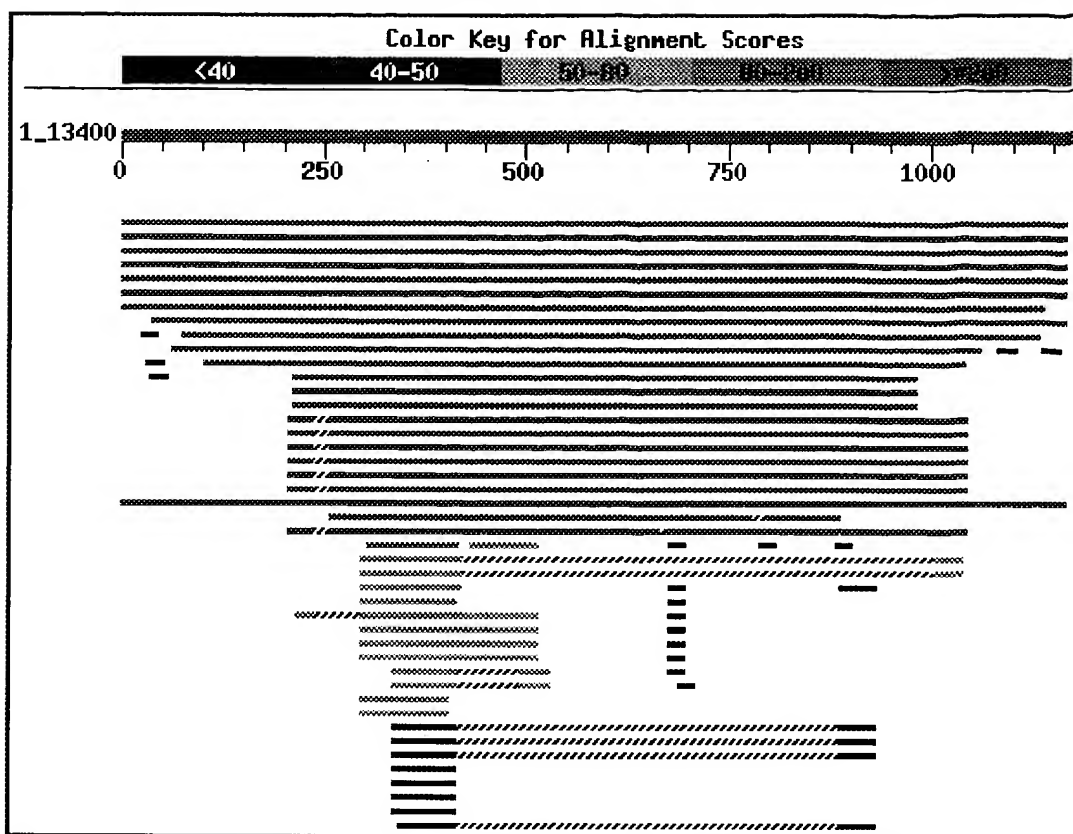
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C Q S +KI L L+A TD + + F RSC EIK
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Query: 241 ECPSAFDGLYFLRTENGVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGS 420
PSA DG+Y L TE+G YQTFCDMT+ GGGWTLVASVHEN+M GKCTVGDRWS+QQG+
Sbjct: 73 SDPSAPDGIYTLATEHGESYQTFCDMTTNGGGWTLVASVHENNMFGKCTVGDRWSTQQGN 132

Query: 421 KADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSL 600
PEGDGNWANY TFG E ATSDDYKNPGYYDIQAK+L +WHVPN +PM +WRNSS+
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Query: 601 LRYRTDTGFLQTLGHNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPY 780
LRYRT F G NLF +Y+KYPVKY GKC DNGP +PVVYD G A+KT+S YSP
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Sequences producing significant alignments:

gi 37181842 gb AY358359.1 	Homo sapiens clone DNA66308 ITLN...	2317	0.0	LU
gi 37724011 gb AY157362.1 	Homo sapiens intelectin (INTL) m...	2317	0.0	LU
gi 44976128 gb AY549722.1 	Homo sapiens omentin mRNA, compl...	2307	0.0	LU
gi 18088357 gb BC020664.1 	Homo sapiens intelectin 1 (galac...	2292	0.0	LUG
gi 31542985 ref NM_017625.2 	Homo sapiens intelectin 1 (gal...	2292	0.0	LUG
gi 37724004 gb AY157361.1 	Homo sapiens intelectin (INTL) m...	2286	0.0	LU
gi 18091782 gb AY065972.1 	Homo sapiens endothelial lectin ...	2248	0.0	LU
gi 7019845 dbj AK000029.1 	Homo sapiens cDNA FLJ20022 fis, ...	2234	0.0	LUG
gi 8096220 dbj AB036706.1 	Homo sapiens Itln mRNA for intel...	2095	0.0	LUG
gi 20377086 gb AF271386.1 	Homo sapiens intestinal lactofer...	1974	0.0	LU
gi 48146564 emb CR457224.1 	Homo sapiens full open reading ...	1855	0.0	
gi 37182927 gb AY358905.1 	Homo sapiens clone DNA108701 ITL...	866	0.0	LU
gi 18091784 gb AY065973.1 	Homo sapiens endothelial lectin ...	866	0.0	LU
gi 37622351 ref NM_080878.2 	Homo sapiens intelectin 2 (ITL...	866	0.0	LU
gi 37724015 gb AY157364.1 	Mus musculus intelectin (Intl) m...	676	0.0	LU
gi 12841003 dbj AK007447.1 	Mus musculus 10 day old male pa...	676	0.0	LUG
gi 37724013 gb AY157363.1 	Mus musculus intelectin (Intl) m...	636	e-179	LU
gi 6754387 ref NM_010584.1 	Mus musculus intelectin (Itln),...	636	e-179	LUG
gi 3357908 dbj AB016496.1 	Mus musculus mRNA for intelectin...	636	e-179	LUG
gi 28932913 gb AY217760.1 	Mus musculus intelectin 2 mRNA, ...	626	e-176	U

gi 22204152 emb AL354714.22	Human DNA sequence from clone ...	551	e-153	
gi 18476709 emb AL591806.16	Human DNA sequence from clone ...	430	e-117	
gi 25046355 gb AC083892.19	Mus musculus chromosome 1 clone...	287	3e-74	
gi 20502360 dbj AB061239.1	Xenopus laevis mRNA for lectin ...	99	1e-17	
gi 41392401 emb BX571811.5	Zebrafish DNA sequence from clo...	73	7e-10	
gi 38564116 emb BX649532.7	Zebrafish DNA sequence from clo...	73	7e-10	
gi 49614137 emb BX284688.12	Zebrafish DNA sequence from cl...	73	7e-10	
gi 49115331 gb BC073311.1	Xenopus laevis cDNA clone MGC:80...	71	3e-09	
gi 49255964 gb BC071079.1	Xenopus laevis cDNA clone MGC:79...	67	5e-08	
gi 2632075 emb X82626.1 XLCORGLEC	X.laevis mRNA for cortica...	67	5e-08	
gi 46040513 dbj BP692558.1	Xenopus laevis NBRP cDNA clone:...	61	3e-06	
gi 1841844 gb U86699.1 XLU86699	Xenopus laevis oocyte lecti...	59	1e-05	
gi 38174755 gb BC061445.1	Xenopus tropicalis hypothetical ...	55	2e-04	
gi 45360436 ref NM_203598.1	Xenopus tropicalis hypotherica...	55	2e-04	
gi 25989471 gb AY079196.1	Xenopus tropicalis egg cortical ...	54	7e-04	
gi 45360964 ref NM_203519.1	Xenopus tropicalis egg cortica...	54	7e-04	
gi 1150691 emb Z50155.1 XLIGF1R	X.laevis mRNA for insulin-l...	52	0.003	
gi 46058673 dbj BP710274.1	Xenopus laevis NBRP cDNA clone:...	48	0.043	
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gi 22266666 dbj AB073013.1	Vitis labrusca x Vitis vinifera...	42	2.6	
gi 22266664 dbj AB073012.1	Vitis labrusca x Vitis vinifera...	42	2.6	
gi 22266660 dbj AB073010.1	Vitis labrusca x Vitis vinifera...	42	2.6	
gi 5442427 gb AF159139.1 AF159139	Gossypium hirsutum phosph...	42	2.6	
gi 47232553 dbj AB111101.1	Vitis vinifera gypsy-type retro...	42	2.6	
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gi 47232545 dbj AB097925.1	Vitis vinifera VvmybA3 mRNA for...	42	2.6	
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gi 47232541 dbj AB097923.1	Vitis vinifera VvmybA1 mRNA for...	42	2.6	
gi 22759512 emb AL772367.7	Mouse DNA sequence from clone R...	42	2.6	
gi 49640134 emb CR382121.1	Kluyveromyces lactis strain NRR...	42	2.6	
gi 46090698 dbj BP742105.1	Xenopus laevis NBRP cDNA clone:...	42	2.6	
gi 46088912 dbj BP740319.1	Xenopus laevis NBRP cDNA clone:...	42	2.6	
gi 46084491 dbj BP735898.1	Xenopus laevis NBRP cDNA clone:...	42	2.6	

Alignment(s)

Get selected sequences

Select all

Deselect all

>gi|37181842|gb|AY358359.1| Homo sapiens clone DNA66308 ITLN (UNQ640) mRNA,
Length = 1176

Score = 2317 bits (1169), Expect = 0.0
Identities = 1169/1169 (100%)
Strand = Plus / Plus

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

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Identities = 1169/1169 (100%)
Strand = Plus / Plus

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Sbjct: 9  agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 68

Query: 61  tgtaccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 120

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Query: 121     ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaatacttacttc 180
|||||
Sbjct: 129     ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaatacttacttc 188

Query: 181     aaggaatggacctgttcttcgtctccatctctgccagaagctgcaaggaaatcaaagac 240
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Sbjct: 189     aaggaatggacctgttcttcgtctccatctctgccagaagctgcaaggaaatcaaagac 248

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Query: 301     cagaccttctgtgacatgacctctgggggtggcggctggacctggtggccagcgtgcat 360
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Score = 2307 bits (1164), Expect = 0.0

Identities = 1167/1168 (99%)

Strand = Plus / Plus

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Query: 61 tgtaccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 120
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Sbjct: 284 aaggaatggacctgttcttcgtctccatctctgcccagaagctgcaaggaaatcaaagac 343

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Sbjct: 344 gaatgtcctagtgcatTTTgatggcctgtatTTTtctccgcaactgagaatgggtgttatctac 403

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Sbjct: 584 gaggcggccacgagcgatgactacaagaaccctggctactacgacatccaggccaaggac 643

Query: 541 ctgggcacatctggcacgtgcccaataagtcccccacgagcactggagaaacagctccctg 600
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Sbjct: 644 ctgggcacatctggcacgtgcccaataagtcccccacgagcactggagaaacagctccctg 703

Query: 601 ctgaggtaccgcacggacactggcttctctccagacactgggacataatctgTTTggcatc 660
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Sbjct: 704 ctgaggtaccgcacggacactggcttctctccagacactgggacataatctgTTTggcatc 763

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Sbjct: 1064 gattggagtgatgatggaactcatgttggttacagcagcagccgtgagataactgaggca 1123

Query: 1021 gctgtgcttctattctatcggttgagagttttgtgggaggggaaccagacctctctccca 1080
 |||



Sbjct: 1124 gctgtgcttctattctatcggttgagagttttgtgggaggggaaccagacctctctccca 1183

Query: 1081 accatgagatcccaaggatggagaacaacttaccagtagctagaatgttaatggcagaa 1140
 |||

Sbjct: 1184 accatgagatcccaaggatggagaacaacttaccagtagctagaatgttaatggcagaa 1243

Query: 1141 gagaaaacaataaatcatattgactcaa 1168
 |||

Sbjct: 1244 gagaaaacaataaatcatattgactcaa 1271

 >gi|18088357|gb|BC020664.1|  Homo sapiens intelectin 1 (galactofuranose bir
 MGC:22348 IMAGE:4693329), complete cds
 Length = 1209

Score = 2292 bits (1156), Expect = 0.0

Identities = 1165/1168 (99%)

Strand = Plus / Plus

Query: 1 agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 60
 |||

Sbjct: 15 agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 74

Query: 61 tgtaccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 120
 |||

Sbjct: 75 tgtaccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 134

Query: 121 ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaatacttacttc 180
 |||

Sbjct: 135 ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaatacttacttc 194

Query: 181 aaggaatggacctgttcttctgtctccatctctgccagaagctgcaaggaaatcaaagac 240
 |||

Sbjct: 195 aaggaatggacctgttcttctgtctccatctctgccagaagctgcaaggaaatcaaagac 254

Query: 241 gaatgtcctagtgcatgttgatggcctgtattttctccgcactgagaatgggtgttatctac 300
 |||

Sbjct: 255 gaatgtcctagtgcatgttgatggcctgtattttctccgcactgagaatgggtgttatctac 314

Query: 301 cagaccttctgtgacatgacctctgggggtggcggtggacctgtgtggccagcgtgcat 360
 |||

Sbjct: 315 cagaccttctgtgacatgacctctgggggtggcggtggaccctggtggccagcgtgcac 374

Query: 361 gagaatgacatgcgtgggaagtgcacgggtgggcgatcgctggtccagtcagcaggggcagc 420
 |||
 Sbjct: 375 gagaatgacatgcgtgggaagtgcacgggtgggcgatcgctggtccagtcagcaggggcagc 434

Query: 421 aaagcagactacccagagggggacggcaactgggccaactacaacacctttggatctgca 480
 |||
 Sbjct: 435 aaagcagtctacccagagggggacggcaactgggccaactacaacacctttggatctgca 494

Query: 481 gaggcggccacgagcgatgactacaagaaccctggctactacgacatccaggccaaggac 540
 |||
 Sbjct: 495 gaggcggccacgagcgatgactacaagaaccctggctactacgacatccaggccaaggac 554

Query: 541 ctgggcacatctggcacgtgccaataagtcccccatgcagcactggagaaacagctccctg 600
 |||
 Sbjct: 555 ctgggcacatctggcacgtgccaataagtcccccatgcagcactggagaaacagctccctg 614

Query: 601 ctgaggtaccgcacggacactggcttctccagacactgggacataatctgtttggcatc 660
 |||
 Sbjct: 615 ctgaggtaccgcacggacactggcttctccagacactgggacataatctgtttggcatc 674

Query: 661 taccagaaatatccagtgaaatatggagaaggaaagtgttgactgacaacggcccggtg 720
 |||
 Sbjct: 675 taccagaaatatccagtgaaatatggagaaggaaagtgttgactgacaacggcccggtg 734

Query: 721 atccctgtggtctatgattttggcgacgccagaaaacagcatcttattactcacctat 780
 |||
 Sbjct: 735 atccctgtggtctatgattttggcgacgccagaaaacagcatcttattactcacctat 794

Query: 781 ggccagcgggaattcactgcgggatttggttcagttcagggtatttaataacgagagagca 840
 |||
 Sbjct: 795 ggccagcgggaattcactgcgggatttggttcagttcagggtatttaataacgagagagca 854

Query: 841 gccaacgccttgtgtgctggaatgagggtcaccggatgtaacactgagcatcactgcatt 900
 |||
 Sbjct: 855 gccaacgccttgtgtgctggaatgagggtcaccggatgtaacactgagcaccactgcatt 914

Query: 901 ggtggaggaggatactttccagaggccagtcgccagcagtggtggagatttttctggtttt 960
 |||
 Sbjct: 915 ggtggaggaggatactttccagaggccagtcgccagcagtggtggagatttttctggtttt 974

Query: 961 gattggagtggatatggaactcatgttggttacagcagcagccgtgagataactgaggca 1020
 |||
 Sbjct: 975 gattggagtggatatggaactcatgttggttacagcagcagccgtgagataactgaggca 1034

Query: 1021 gctgtgcttctattctatcggttgagagttttgtgggaggggaacccagacctctcctcca 1080
 |||